

## SEQUENCE LISTING

- <110> Genentech, Inc.  
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Wood, William, I.
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- <140> 09/665,350  
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- <150> PCT/US00/04414  
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- <150> US 60/145,698  
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- <150> US 60/146,222  
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- <150> PCT/US99/20594  
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- <150> PCT/US99/20944  
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<213> Homo sapiens

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
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Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
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Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
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Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
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Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
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<212> PRT

<213> Homo sapiens

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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 <223> Description of Artificial Sequence: Synthetic  
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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
 35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
 50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
 65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
 85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
 100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
 115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
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His Asp Pro Gly

"GOLD" TEST

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<211> 22

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<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens







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<211> 28

<212> DNA

 $\langle 220 \rangle$ 

<400> 24

<210> 25

<211> 24  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<210> 26  
 <211> 41  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
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 <223> a, t, c or g

<400> 26  
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<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

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<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
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Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
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Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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46

<210> 33

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<212> DNA

<213> Homo sapiens

<400> 33

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<212> PRT
<213> Homo sapiens
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Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
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Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
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Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
145 150 155 160

Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
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Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
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Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

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Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
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Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln Asp	Leu Cys Ala Met	Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn Val	Pro Gly Ser Phe	Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala Glu	Asp Gly Lys Arg	Cys Val Ala			
305	310	315	320			
Val Asp Tyr Cys	Ala Ser Glu Asn His	Gly Cys Glu His	Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys Gln	Cys His Glu Gly	Phe Ala Leu			
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Asn Pro Asp Glu	Lys Thr Cys Thr Arg	Ile Asn Tyr Cys	Ala Leu Asn			
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Lys Pro Gly Cys	Glu His Glu Cys Val	Asn Met Glu Glu	Ser Tyr Tyr			
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385	390	395	400			
Ser Arg Val Asp	His Cys Ala Gln Gln	Asp His Gly Cys	Glu Gln Leu			
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Cys Leu Asn Thr	Glu Asp Ser Phe Val	Cys Gln Cys Ser	Glu Gly Phe			
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Leu Ile Asn Glu	Asp Leu Lys Thr Cys	Ser Arg Val Asp	Tyr Cys Leu			
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Leu Ser Asp His	Gly Cys Glu Tyr Ser	Cys Val Asn Met	Asp Arg Ser			
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Phe Ala Cys Gln	Cys Pro Glu Gly His	Val Leu Arg Ser	Asp Gly Lys			
465	470	475	480			
Thr Cys Ala Lys	Leu Asp Ser Cys Ala	Leu Gly Asp His	Gly Cys Glu			
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His Ser Cys Val	Ser Ser Glu Asp Ser	Phe Val Cys Gln	Cys Phe Glu			
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 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
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 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
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 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
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 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
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 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
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 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
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 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
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 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
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<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 37

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45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

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<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu



Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
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Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

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24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
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 <213> Artificial Sequence  
  
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 oligonucleotide probe  
  
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 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
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 oligonucleotide probe  
  
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 <210> 46  
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 oligonucleotide probe  
  
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 <210> 47



<211> 45  
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 oligonucleotide probe

<400> 47  
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<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

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<210> 49
<211> 690
<212> PRT
<213> Homo sapiens

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Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
          35              40              45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
  50              55              60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
  65              70              75              80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
          85              90              95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
          100              105              110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
          115              120              125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
          130              135              140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
          145              150              155              160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
          165              170              175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

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T02T0202940660

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Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys		
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Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe		
225			230						235			240					
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys		
			245						250			255					
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met		
			260						265			270					
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala		
275						280						285					
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser		
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Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln		
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Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile		
			325						330			335					
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys		
			340			345						350					
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser		
355						360						365					
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp		
370			375						380								
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser		
385			390						395			400					
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly		
			405						410			415					
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln		
			420			425						430					
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr		
435						440						445					
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys		
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<223> a, t, c or g

<400> 50

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tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

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<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

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ggagtagaaa gcgcatgg 18

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<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

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cacctgatac catgaatggc ag 22

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<210> 54

<211> 18

<212> DNA

<220>

<400> 54

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<400> 55

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<400> 56

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<400> 57

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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gggacaagaa gccgcccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60











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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
50 55 60



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Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn	
		355					360					365				
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr	
	370					375					380					
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro	
385					390					395					400	
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met	
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Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu	
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Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala	
		435					440					445				
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu	
	450					455					460					
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr	
465					470					475					480	
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys	
				485					490					495		
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys	
			500					505					510			
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys	
		515					520					525				
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser	
	530					535					540					
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr	
545				550					555						560	
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys	
				565					570					575		
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys	
			580					585					590			
Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn	
		595					600					605				
Val	Thr	Thr	Lys	Gly	Leu	His	Pro	Asp	Gln	Lys	Glu	Tyr	Glu	Lys	Asn	
	610					615					620					

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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tcttctctct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420
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```

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

T00120"29440660







Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	Gln	Leu	Val	Gly
305					310					315					320
Gly	Gln	Leu	Ala	Val	Val	Glu	Pro	Tyr	Ala	Phe	Arg	Gly	Leu	Asn	Tyr
				325					330					335	
Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	Leu	Glu	Glu
			340					345					350		
Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	Leu	Asp	Ser
		355					360					365			
Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	Arg	Arg	Arg
	370					375					380				
Trp	Arg	Leu	Asn	Phe	Asn	Arg	Gln	Gln	Pro	Thr	Cys	Ala	Thr	Pro	Glu
385					390					395					400
Phe	Val	Gln	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	Leu	Leu	Pro
				405					410				415		
Asn	Tyr	Phe	Thr	Cys	Arg	Arg	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Ala	Gln
			420					425					430		
Gln	Val	Phe	Val	Asp	Glu	Gly	His	Thr	Val	Gln	Phe	Val	Cys	Arg	Ala
		435					440					445			
Asp	Gly	Asp	Pro	Pro	Pro	Ala	Ile	Leu	Trp	Leu	Ser	Pro	Arg	Lys	His
	450					455					460				
Leu	Val	Ser	Ala	Lys	Ser	Asn	Gly	Arg	Leu	Thr	Val	Phe	Pro	Asp	Gly
465					470					475					480
Thr	Leu	Glu	Val	Arg	Tyr	Ala	Gln	Val	Gln	Asp	Asn	Gly	Thr	Tyr	Leu
				485					490					495	
Cys	Ile	Ala	Ala	Asn	Ala	Gly	Gly	Asn	Asp	Ser	Met	Pro	Ala	His	Leu
			500					505					510		
His	Val	Arg	Ser	Tyr	Ser	Pro	Asp	Trp	Pro	His	Gln	Pro	Asn	Lys	Thr
		515					520					525			
Phe	Ala	Phe	Ile	Ser	Asn	Gln	Pro	Gly	Glu	Gly	Glu	Ala	Asn	Ser	Thr
	530					535					540				
Arg	Ala	Thr	Val	Pro	Phe	Pro	Phe	Asp	Ile	Lys	Thr	Leu	Ile	Ile	Ala
545					550					555					560
Thr	Thr	Met	Gly	Phe	Ile	Ser	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Leu
				565					570					575	
Val	Leu	Leu	Phe	Leu	Trp	Ser	Arg	Gly	Lys	Gly	Asn	Thr	Lys	His	Asn

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
610 615 620

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<400> 75
ataccagcta taaccaggct gcg                                     23
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<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<400> 76
caacagtaag tggtttgatg ctcttcctaaa tctagagatt ctgatgattg 50
gg 52
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```
<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 77  
 ccatgtgtct cctcctacaa ag 22

<210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 78  
 gggaatagat gtgatctgat tgg 23

<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 79  
 cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 80  
 agcaaccgcc tgaagctcat cc 22

<210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 81  
 aaggcgcggt gaaagatgta gacg 24

<210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 ccacgcgctc cgcacctcgg ccccgggctc cgaagcggct cggggggcgcc ctttcgggtca 60  
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 agccagggag cgggcccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180  
 tcttgcgtgt cgcctgctgc tgggcgcccc gcgggggccaa cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtggccaag 300  
 tgaaagatca cgaggactca tccctgcaat ggtctaacct tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct gggtacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaagt cctcctgcac tgtgctagga attccacaga 540  
 agcccatcat cactgggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
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 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met	Gly	Ala	Pro	Ala	Ala	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Ala
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Cys	Cys	Trp	Ala	Pro	Gly	Gly	Ala	Asn	Leu	Ser	Gln	Asp	Asp	Ser	Gln
			20					25					30		
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu
		35					40					45			
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn
	50					55					60				
Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp
65					70					75					80
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser
				85					90					95	
Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile
		100						105					110		
Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly
		115					120					125			
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu
	130					135					140				
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala
145					150					155					160
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro
				165					170					175	
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser
			180					185					190		
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val
		195					200				205				
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser
	210					215					220				
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp
225					230					235					240
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly
				245					250					255	
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser
			260					265					270		
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe
		275					280					285			

<223> Description of Artificial Sequence: Synthetic



## oligonucleotide probe

<400> 87  
cctagcacag tgacgaggga cttggc 26

<210> 88  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 88  
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 89  
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90  
<211> 2755  
<212> DNA  
<213> Homo sapiens

<400> 90  
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1                      5                      10                      15

```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
          20                      25                      30

```

```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
          35                      40                      45

```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
          50                      55                      60

```

```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
          65                      70                      75                      80

```

```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
          85                      90                      95

```



Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
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 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
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 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
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 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
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 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
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 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
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 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
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 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
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 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

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Trp	His	Asn	Gly	Pro	Tyr	Asn	Ala	Asp	Gly	Ala	His	Arg	Val	Tyr	Asp
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<212>	DNA														
<213>	Homo sapiens														
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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg 65	Ala	Gly	Ala	Glu	Leu	Arg	Ala	Val	Leu	Ala	Leu	Leu	Arg	Ala	Gly 80				
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Pro	Gly	Pro	Gly	Gly	Gly	Ser	Lys	Asp	Leu	Leu	Phe	Trp	Val	Ala	Leu				
				85				90				95							
Glu	Arg	Arg	Arg	Ser	His	Cys	Thr	Leu	Glu	Asn	Glu	Pro	Leu	Arg	Gly				
				100				105				110							
Phe	Ser	Trp	Leu	Ser	Ser	Asp	Pro	Gly	Gly	Leu	Glu	Ser	Asp	Thr	Leu				
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Gln	Trp	Val	Glu	Glu	Pro	Gln	Arg	Ser	Cys	Thr	Ala	Arg	Arg	Cys	Ala				
				130				135				140							
Val 145	Leu	Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met 160				
				150				155											
Arg	Cys	His	Leu	Arg	Ala	Asn	Gly	Tyr	Leu	Cys	Lys	Tyr	Gln	Phe	Glu				
				165				170				175							
Val	Leu	Cys	Pro	Ala	Pro	Arg	Pro	Gly	Ala	Ala	Ser	Asn	Leu	Ser	Tyr				
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Arg	Ala	Pro	Phe	Gln	Leu	His	Ser	Ala	Ala	Leu	Asp	Phe	Ser	Pro	Pro				
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Gly	Thr	Glu	Val	Ser	Ala	Leu	Cys	Arg	Gly	Gln	Leu	Pro	Ile	Ser	Val				
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Thr 225	Cys	Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly 240				
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Asp	Val	Leu	Cys	Pro	Cys	Pro	Gly	Arg	Tyr	Leu	Arg	Ala	Gly	Lys	Cys				
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Ala	Glu	Leu	Pro	Asn	Cys	Leu	Asp	Asp	Leu	Gly	Gly	Phe	Ala	Cys	Glu				
				260				265				270							
Cys	Ala	Thr	Gly	Phe	Glu	Leu	Gly	Lys	Asp	Gly	Arg	Ser	Cys	Val	Thr				
				275				280				285							
Ser 290	Gly	Glu	Gly	Gln	Pro	Thr	Leu	Gly	Gly	Thr	Gly	Val	Pro	Thr	Arg				
				295				300											
Arg 305	Pro	Pro	Ala	Thr	Ala	Thr	Ser	Pro	Val	Pro	Gln	Arg	Thr	Trp	Pro 320				
				310				315											
Ile	Arg	Val	Asp	Glu	Lys	Leu	Gly	Glu	Thr	Pro	Leu	Val	Pro	Glu	Gln				
				325				330				335							
Asp	Asn	Ser	Val	Thr	Ser	Ile	Pro	Glu	Ile	Pro	Arg	Trp	Gly	Ser	Gln				

340                                      345                                      350  
 Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala  
                  355                                      360                                      365  
 Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr  
                  370                                      375                                      380  
 Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe  
 385                                      390                                      395                                      400  
 Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr  
    405                                      410                                      415  
 Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln  
    420                                      425                                      430  
 Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu  
    435                                      440                                      445  
 Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val  
    450                                      455                                      460  
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<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 97

tggaaggaga tgcgatgcca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20



<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgcgcgct      50
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<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens
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Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	395
400		
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

T00T00"09440660

<213> Homo sapiens

<400> 108

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<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20             25             30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35             40             45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50             55             60

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Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
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<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

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50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

TOP 20 "2944000000

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
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<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45



Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
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 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
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agcaactctt cctatgtcct gaatcccaca acaggagagc tggctcttga tccccgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
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<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

```

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1                      5                      10                      15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
                20                      25                      30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
                35                      40                      45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
                50                      55                      60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
                65                      70                      75                      80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
                85                      90                      95

```



<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 125

20

<210> 126

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 126

cagcgcgtgg	ccggcgccgc	tgtggggaca	gcatagagcgg	cgggtggatg	gcgcaggttg	60
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gcctgtaggc	cgccgcgagc	cgctttcca	ccccgacctc	tgcacaggcc	gcaggcccca	180
gctcaggctc	gtgccacccc	accaagttcc	agtgccgcac	cagtggctta	tgcgtgcccc	240
tcacctggcg	ctgcgacagg	gacttggact	gcagcgatgg	cagcgatgag	gaggagtgca	300
ggattgagcc	atgtacccag	aaagggcaat	gcccacccgc	ccctggcctc	ccctgcccct	360
gcaccggcgt	cagtgactgc	tctgggggaa	ctgacaagaa	actgcgcaac	tgcagccgcc	420
tggcctgcct	agcaggcgag	ctccgttgca	cgctgagcga	tgactgcatt	ccactcacgt	480
ggcgctgcga	cggccaccca	gactgtcccg	actccagcga	cgagctcggc	tgtggaacca	540
atgagatcct	cccggaaggg	gatgccacaa	ccatggggcc	ccctgtgacc	ctggagagtg	600
tcacctctct	caggaatgcc	acaacccatg	ggccccctgt	gaccctggag	agtgtcccct	660
ctgtcgggaa	tgccacatcc	tctctgccc	gagaccagtc	tggaaagcca	actgcctatg	720
gggttattgc	agctgctgcg	gtgctcagtg	caagcctggt	caccgccacc	ctcctccttt	780
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agtccctgct	gctgtcagaa	cagaagacct	cgctgccctg	aggacaagca	cttgccacca	900
ccgtcactca	gccttgggcg	tagccggaca	ggaggagagc	agtgatcggg	atgggtacct	960
gggcacacca	gccttcagag	acctgagttc	ttctggccac	gtggaacctc	gaaccgagc	1020
tcttcagaaa	gtggccctgg	agattgaggg	tccttgagca	ctccctatgg	agatccgggg	1080
agctaggatg	gggaacctgc	cacagccaga	actgaggggc	tggccccagg	cagctcccag	1140
gggttagaac	ggccctgtgc	ttaagacact	ccctgctgcc	ccgtctgagg	gtggcgatta	1200
aaqttgcttc						1210

<210> 127

<211> 282

&lt;212&gt; PRT

<213> Homo sapiens

<400> 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

Ser	Asp	Gly	Ser	Asp	Glu	Glu	Glu	Cys	Arg	Ile	Glu	Pro	Cys	Thr	Gln	
				85					90					95		
Lys	Gly	Gln	Cys	Pro	Pro	Pro	Pro	Gly	Leu	Pro	Cys	Pro	Cys	Thr	Gly	
				100					105					110		
Val	Ser	Asp	Cys	Ser	Gly	Gly	Thr	Asp	Lys	Lys	Leu	Arg	Asn	Cys	Ser	
				115					120					125		
Arg	Leu	Ala	Cys	Leu	Ala	Gly	Glu	Leu	Arg	Cys	Thr	Leu	Ser	Asp	Asp	
				130					135					140		
Cys	Ile	Pro	Leu	Thr	Trp	Arg	Cys	Asp	Gly	His	Pro	Asp	Cys	Pro	Asp	
				145					150					155		
Ser	Ser	Asp	Glu	Leu	Gly	Cys	Gly	Thr	Asn	Glu	Ile	Leu	Pro	Glu	Gly	
				165					170					175		
Asp	Ala	Thr	Thr	Met	Gly	Pro	Pro	Val	Thr	Leu	Glu	Ser	Val	Thr	Ser	
				180					185					190		
Leu	Arg	Asn	Ala	Thr	Thr	Met	Gly	Pro	Pro	Val	Thr	Leu	Glu	Ser	Val	
				195					200					205		
Pro	Ser	Val	Gly	Asn	Ala	Thr	Ser	Ser	Ser	Ala	Gly	Asp	Gln	Ser	Gly	
				210					215					220		
Ser	Pro	Thr	Ala	Tyr	Gly	Val	Ile	Ala	Ala	Ala	Ala	Val	Leu	Ser	Ala	
				225					230					235		
Ser	Leu	Val	Thr	Ala	Thr	Leu	Leu	Leu	Leu	Ser	Trp	Leu	Arg	Ala	Gln	
				245					250					255		
Glu	Arg	Leu	Arg	Pro	Leu	Gly	Leu	Leu	Val	Ala	Met	Lys	Glu	Ser	Leu	
				260					265					270		
Leu	Leu	Ser	Glu	Gln	Lys	Thr	Ser	Leu	Pro							
				275					280							

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129











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ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaataatt 720
ctgatgagaa accagcagtt ctttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgcca aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattcccctt ctctcctcc 900
ttgtggctac cacagttgta tgttgggttt ggtctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
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atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

&lt;210&gt; 138

115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaaggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctccctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgtactg 240  
 cctgcaccag cggcgggtgg cctggccga gctgcaggag gccgatggcc agtgtccggg 300  
 cgaccgcagc ctgctgaagt tgaaaatggg gcaggctcgtg tttcgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtgggc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc ttccaccaac cttcaaccca caggaggtct ttattcgttc 660  
 cactaacatt tttcgggaatc tggagtccac ccgttggttg ctggctgggc tttccagtg 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
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attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
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gaccctgggg atttttgacc acaaattggc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

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<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1                      5                      10                      15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20                      25                      30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35                      40                      45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
      50                      55                      60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
      65                      70                      75                      80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85                      90                      95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
      100                      105                      110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
      115                      120                      125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
      130                      135                      140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
      145                      150                      155                      160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165                      170                      175

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gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtatatt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccacaga 480
gagctctttc tccccagtc cagagggtgt caggctggct gacggccctg ggcattgcaa 540
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cctccggggc gcaaaggtgg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaacc ttcaggattg cccttctggg ccttggggga agaacacctg 780
caacctgatg gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
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tccacattgc acacagcaga tcccagcct ccataattgt gtgtatcaac tacttaata 1440
cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500
tgthttctctg aagaactctg aaaaaatata gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt gggtatgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggttaact tatttacaat aataaagata gcactatgtg 1680
ttcaaa

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<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110



## oligonucleotide probe

<400> 149  
ttcagctcat caccttcacc tgcc 24

<210> 150  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 150  
ggctcatata aaataccact aggg 24

<210> 151  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 151  
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152  
<211> 1427  
<212> DNA  
<213> Homo sapiens

<400> 152  
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60  
accacgcgt ccgcggacgc gtgggaggac gcggtggccg gctaccagga agagtctgcc 120  
gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180  
cctgggcgtc ttcggcctct tccggtgct gcagtgggtg cgcgggaagg cctacctgcg 240  
gaatgctgtg gtggtgatca caggcgccac ctcagggtg ggcaaagaat gtgcaaaagt 300  
cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360  
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1             5             10             15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
          20             25             30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
      35             40             45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
      50             55             60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
      65             70             75             80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
          85             90             95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
      100            105            110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
      115            120            125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
      130            135            140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
      145            150            155            160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
          165            170            175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
      180            185            190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
      195            200            205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

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210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235 240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
	245	250 255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
	260	265 270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
	275	280 285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
	290	295 300
Arg Lys Ser Lys Asn Ser		
305	310	

&lt;210&gt; 154

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 154

ggtgctaaac tgggtgctctg tggc

24

&lt;210&gt; 155

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 155

cagggcaaga tgagcattcc

20

&lt;210&gt; 156

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

T00120" 29440660

<400> 156  
tcatactgtt ccatctcggc acgc 24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gtcctcaga gaactcaccg cttctcatgc 50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
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cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1771

<210> 159





Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 160

ggatgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttgttt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

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cccacgcgcgc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcgcgcggc 60
tcaqqqaqqa qcaccgactg cgcgcgaccc tgagagatgg ttggtgccat gtggaagggtg 120
```





Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165

ttccatgcca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

agctctcaga ggctgggtcat aggg

24

<211> 50

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<211> 2477

<213> Homo sapiens

cgagggcttt	tccggctccg	gaatggcaca	tgtgggaatc	ccagtcttgt	tggctacaac	60
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tcttgctgga	gaagaaaggg	ctgagggcag	agcagggcac	tctcactcag	ggtgaccagc	180
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cctggagagc	ctgggggagg	gcctgcctaa	caagctttca	aaaaacagga	gcgacttcca	360
ctgggctggg	ataagacgtg	ccggtaggat	agggaaagact	gggttttagtc	ctaatatcaa	420
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Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
 1             5             10             15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
      20             25             30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
      35             40             45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
      50             55             60

```

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Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
      65             70             75             80

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```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
      85             90             95

```

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Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
      100            105            110

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Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
      115            120            125

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Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
      130            135            140

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Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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aaggggagca aagccgggct cggcccagg ccccaggac ctccatctcc caatgttgga 180  
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaacgcca 240  
tggtcccaa gaagctgtcc tgccttcgtt cctgctgct gccgctcagc ctgacgtac 300  
tgctgcccc ggcagacact cggtcgttcg tagtggatag gggtcatgac cgtttctcc 360  
tagacggggc cccgttcgcg tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

176 2505 DNA Homo sapiens

tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480  
 atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540  
 acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600  
 gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720  
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 ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840  
 tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900  
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960  
 ctgacaacat gaccaaatac tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020  
 taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggg 1080  
 ctgtgtcagc tgtaaccaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140  
 tgtacatgtt ccatggaggt accaactttg gatattggaa tgggtgccgat aagaagggac 1200  
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 ggtggctcat gctgtgaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280  
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 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp	Arg	Leu	Leu	Lys	Met	Arg	Trp	Ser	Gly	Leu	Asn	Ala	Ile	Gln	Phe	65	70	75	80
Tyr	Val	Pro	Trp	Asn	Tyr	His	Glu	Pro	Gln	Pro	Gly	Val	Tyr	Asn	Phe	85	90	95	
Asn	Gly	Ser	Arg	Asp	Leu	Ile	Ala	Phe	Leu	Asn	Glu	Ala	Ala	Leu	Ala	100	105	110	
Asn	Leu	Leu	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ala	Glu	Trp	115	120	125	
Glu	Met	Gly	Gly	Leu	Pro	Ser	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Ile	His	130	135	140	
Leu	Arg	Thr	Ser	Asp	Pro	Asp	Phe	Leu	Ala	Ala	Val	Asp	Ser	Trp	Phe	145	150	155	160
Lys	Val	Leu	Leu	Pro	Lys	Ile	Tyr	Pro	Trp	Leu	Tyr	His	Asn	Gly	Gly	165	170	175	
Asn	Ile	Ile	Ser	Ile	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala	180	185	190	
Cys	Asp	Phe	Ser	Tyr	Met	Arg	His	Leu	Ala	Gly	Leu	Phe	Arg	Ala	Leu	195	200	205	
Leu	Gly	Glu	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Asp	Gly	Pro	Glu	Gly	Leu	210	215	220	
Lys	Cys	Gly	Ser	Leu	Arg	Gly	Leu	Tyr	Thr	Thr	Val	Asp	Phe	Gly	Pro	225	230	235	240
Ala	Asp	Asn	Met	Thr	Lys	Ile	Phe	Thr	Leu	Leu	Arg	Lys	Tyr	Glu	Pro	245	250	255	
His	Gly	Pro	Leu	Val	Asn	Ser	Glu	Tyr	Tyr	Thr	Gly	Trp	Leu	Asp	Tyr	260	265	270	
Trp	Gly	Gln	Asn	His	Ser	Thr	Arg	Ser	Val	Ser	Ala	Val	Thr	Lys	Gly	275	280	285	
Leu	Glu	Asn	Met	Leu	Lys	Leu	Gly	Ala	Ser	Val	Asn	Met	Tyr	Met	Phe	290	295	300	
His	Gly	Gly	Thr	Asn	Phe	Gly	Tyr	Trp	Asn	Gly	Ala	Asp	Lys	Lys	Gly	305	310	315	320
Arg	Phe	Leu	Pro	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Ser	325	330	335	
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile				

				340						345						350	
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Ser	Pro	
		355					360					365					
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu		
	370					375					380						
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu		
385					390					395					400		
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr		
				405				410						415			
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val		
			420					425					430				
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val		
		435					440					445					
Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr		
	450					455					460						
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg		
465					470					475					480		
Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro		
				485				490						495			
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu		
			500					505					510				
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys		
		515					520					525					
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr		
	530					535					540						
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly		
545					550					555					560		
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr		
				565					570					575			
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu		
			580					585					590				
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu		
		595					600					605					
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu		
	610					615					620						





<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182

tggcaccag aatggtgttg gctc

24

<210> 183

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183

cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 184

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 gcaccacaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattatatt 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctggtt attcaggata cttttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcggt 300  
 ttggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420  
 tgcactgtgt catgctgtcg ggggtgccc atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600  
 ttcttcgcca tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc cttaagaaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag ttacagaaa ctcagatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaag tggacattct gccaaaacaa ttgttttaaa 1320



Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

```
<400> 189
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acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccttggg 120
aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcctcccttg 180
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acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgcctt 240  
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 atcgttgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360  
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 cacaacccag acaaggtgtg gtgggccaaag aacagccagg ccaaaaccat tgccacggag 480  
 tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
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 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
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 cagctgcttg agatccctac agagagcttc cactgggggc aacccttcca ggaaggagtt 780  
 ggggagagag aaccctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
 ctcacacaaa tctacccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
 gctgatgtaa cacagagcct ataaaagctg tgggtcctta aggctgcccc gcgccttgcc 960  
 aaaatggagc ttgtaagaag gctcatgcc a ttgacctct taattctctc ctgtttggcg 1020  
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 aatatggcag agaccacaaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
 tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttccta tgtccagctt 1200  
 gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260  
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 aatgtgggtg ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
 aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820  
 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggctgaaag tgacacacag gctgcatgt aaaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

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 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
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 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285



565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
595 600 605

<210> 191  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 191  
tctctattcc aaactgtggc g 21

<210> 192  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 192  
tttgatgacg attcgaaggt gg 22

<210> 193  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 193  
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
<211> 2362  
<212> DNA  
<213> Homo sapiens

<400> 194  
gacggaagaa cagcgctccc gaggccgagg gagcctgcag agaggacagc cggcctgcgc 60  
cgggacatgc ggccccagga gctccccagg ctgcggttcc cggtgctgct gttgctgttg 120  
ctgctgctgc cgccgcgcgc gtgccctgcc cacagcgcca cgcgcttcga cccacctgg 180









<400>	200					
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catctgaggt	gtttccctgg	ctctgaaggg	gtaggcacga	tggccagggtg	cttcagcctg	180
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gcgaaccagc	agctgaattt	cacagaagct	aaggaggcct	gtaggctgct	gggactaagt	360
ttggccggca	aggaccaagt	tgaaacagcc	ttgaaagcta	gctttgaaac	ttgcagctat	420
ggctgggttg	gagatggatt	cgtggctcat	tctaggatta	gcccacaacc	caagtgtggg	480
aaaaattggg	tgggtgtcct	gatttggaa	gttccagtga	gccgacagtt	tgcagcctat	540
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tcaggactgc	catctggacta	tggagtcgac	caaagagaat	gccttctctc	ttattgtaac	1320
cctgtctgga	tcctatcttc	ttacctccaa	agcttcccac	ggccttttcta	gcctggctat	1380
gtcctaataa	tatcccactg	ggagaaagga	gttttgcaaa	gtgcaaggac	ctaaaacatc	1440

```

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctagggtg ggttgaaagc 1500
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atacctaaga agtacattgt tacctctata taccaaagca catttttaaaa gtgccattaa 2280
caaatgtatc actagccttc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca ttagaaaaac tt 2372

```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

```

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1              5              10              15

```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20              25              30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35              40              45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50              55              60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65              70              75              80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85              90              95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100             105             110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115             120             125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130             135             140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
165 170 175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
225 230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
245 250 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
260 265 270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
275 280 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
290 295 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
305 310 315 320

Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence



&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

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ggctcgccca accttactac cttctgtcgg ccctgtcttc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggt aaccggtgtg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgata ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccac ccctatatat gggccctgag tatatcaagt 420
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tggagtctct tgccaattgg tctaataact gccaatcatt tgcccctatc tatgtgacc 540
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gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatagagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
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gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
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gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttgaggga gaaatcccct ggactttcac taaccctctg 1560
acatactccc cacaccagat tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1             5             10             15

```

```

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
      20             25             30

```

```

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
      35             40             45

```

```

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
      50             55             60

```

```

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
      65             70             75             80

```



Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys  
290 295

&lt;210&gt; 208

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 208

gcttggatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
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 tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120  
 cccattgctc ctgtgcccg gtcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcggc aacgaccaga acctaggcaa cggatcatggc aaagacctcc ttaatggagt 240  
 gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
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 atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420  
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 agggggccctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccaa 1860  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980  
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr  
 1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr 130 135 140		
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu 145 150 155 160		
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg 165 170 175		
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala 180 185 190		
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly 195 200 205		
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr 210 215 220		
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro 225 230 235 240		
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp 245 250 255		
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu 260 265 270		
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu 275 280 285		
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys 290 295 300		
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser 305 310 315 320		
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu 325 330 335		
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr 340 345 350		
Gly Val Tyr Cys Tyr Arg Gln His 355 360		

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

T02F20"29440660

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215

ttcccttggtg gggtggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217

agccagtgag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180  
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 cgcgggggac ggcgacggct ggggtgtcgt ggcgagctt cgcgctgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcgggtgag cgcgccctgg gacacgtacg acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540  
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 agccttcctg cccccgagg agttccctca catgcgggac atcgtgattg ctgaaacct 660  
 ggaggacctg gacagaaaca aagatggcta tgtccagggtg gaggagtaca tcgcggatct 720  
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840  
 ggtgctgccc cctgcccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900  
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960  
 tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020  
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 tgcttggcct ggcttgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440  
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 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

FOET-20-29440600





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44

<210> 226  
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 <212> DNA  
 <213> Homo sapiens

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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<210> 233  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 233  
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<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

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<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
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Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
 65 70 75 80







<210> 242  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
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24

<210> 243  
 <211> 45  
 <212> DNA  
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<220>  
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45

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Ala Ser Gly Glu	Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu			
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Pro Glu Pro Glu	Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu			
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Thr Pro Ala His	Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly			
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Thr Leu Glu Leu	Arg Arg Val Thr Ala	Glu Glu Ala Gly Leu Tyr			
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Thr Cys Val Ala	Gln Asn Leu Val Gly	Ala Asp Thr Lys Thr Val			
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Ser Val Val Val	Gly Arg Ala Leu Leu	Gln Pro Gly Arg Asp Glu			
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Gly Gln Gly Leu	Glu Leu Arg Val Gln	Glu Thr His Pro Tyr His			
	530		535		540
Ile Leu Leu Ser	Trp Val Thr Pro Pro	Asn Thr Val Ser Thr Asn			
	545		550		555
Leu Thr Trp Ser	Ser Ala Ser Ser Leu	Arg Gly Gln Gly Ala Thr			
	560		565		570
Ala Leu Ala Arg	Leu Pro Arg Gly Thr	His Ser Tyr Asn Ile Thr			
	575		580		585
Arg Leu Leu Gln	Ala Thr Glu Tyr Trp	Ala Cys Leu Gln Val Ala			
	590		595		600
Phe Ala Asp Ala	His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr			
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Lys Glu Ala Thr	Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly			
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Leu Ile Ala Ile	Leu Ala Leu Ala Val	Leu Leu Leu Ala Ala Gly			
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Leu Ala Ala His	Leu Gly Thr Gly Gln	Pro Arg Lys Gly Val Gly			
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Gly Arg Arg Pro	Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser			
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Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
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Leu Pro Pro Leu Ser Gln Asn Ser  
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<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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<211> 546

<212> PRT

<213> Homo Sapien

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Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
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Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
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				80					85				90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys

				95					100					105
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro
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Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu
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Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp
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Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu
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Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp
				170					175					180
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val
				185					190					195
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu
				200					205					210
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala
				215					220					225
Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp
				230					235					240
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu
				245					250					255
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr
				260					265					270
Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu
				275					280					285
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp
				290					295					300
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr
				305					310					315
Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr
				320					325					330
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser
				335					340					345
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn
				350					355					360



<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 252  
 gatggctagg ttctggaggt tctg 24

<210> 253  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 253  
 caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254  
 <211> 1650  
 <212> DNA  
 <213> Homo Sapien

<400> 254  
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 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200  
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 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
				20					25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	50	55	60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	65	70	75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	80	85	90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	95	100	105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	110	115	120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	125	130	135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	140	145	150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	155	160	165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	170	175	180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	185	190	195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	200	205	210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	215	220	225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	230	235	240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	245	250	255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	260	265	270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	275	280	285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	290	295	300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly			

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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cggttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgcgc tgctcagcca ccgctgggca 250

ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300

cgggtggatg gtccagtttg gccagctgac ttccatgcc tcttcttgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400



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 cccctcctgg ccactactct tttccctct tctctgggct ctcccactcc 950  
 tggggccggg ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000  
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 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg  
           1                  5                  10                  15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser  
                           20                  25                  30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly  
                           35                  40                  45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg  
                           50                  55                  60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg  
                           65                  70                  75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu  
                           80                  85                  90

"BTE" 2940550



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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr



Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly
				290					295					300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser
				305					310					315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp
				320					325					330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met
				335					340					345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp
				350					355					360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg
				365					370					375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly
				380					385					390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp
				395					400					405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser
				410					415					420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His
				425					430					435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro
				440					445					450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg
				455					460					465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val
				470					475					480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser
				485					490					495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln
				500					505					510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser
				515					520					525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro
				530					535					540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu
				545					550					555

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	3500	1500	1000	8000
Health status	0.5	0.5	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	4.5	1.5	1	7
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Depression score	10.5	5.5	0	30
Anxiety score	12.5	6.5	0	35
Quality of life score	75.5	15.5	50	100









<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
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 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtggggcg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300  
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 cgggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450  
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 ttccatcat cgactcgga gtctgcagcc atctgtactg gcggggagca 700  
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 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
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 aataggetca tctacctata cctctggggg cccggacggc tgctgcggaa 1150

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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
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<211> 24

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<211> 19

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<210> 266

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<210> 282

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atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

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Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu  
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 Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr  
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 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly  
 170 175 180  
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser  
 185 190 195  
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 200 205 210  
 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser  
 215 220 225  
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile  
 230 235 240  
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 245 250 255  
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 260 265 270  
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 275 280 285  
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu  
 290 295 300  
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile  
 305 310 315  
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 320 325 330  
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly  
 335 340 345  
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu  
 350 355 360  
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro  
 365 370 375  
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr  
 380 385 390  
 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser  
 395 400 405







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<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25					30







Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560		565	570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575		580	585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590		595	600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605		610	615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620		625	630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635		640	645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650		655	660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665		670	675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680		685	690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695		700	705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710		715	720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725		730	735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740		745	750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755		760	765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770		775	780
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Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
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Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
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 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
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 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
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 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
 1010 1015 1020  
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
 1025 1030 1035  
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&lt;210&gt; 291

&lt;211&gt; 2906

PDB: 2Q9H



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Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His	290		295		300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp	305		310		315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys	320		325		330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp	335		340		345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp	410		415		420

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TOE 20 29440000









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<213> Homo Sapien

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg  
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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Lys Ile Lys Asn Val Asp Gly Leu Thr	Phe Gln Gly Leu Gly Ala				
230	235	240			
Leu Lys Ser Leu Lys Met Gln Arg Asn	Gly Val Thr Lys Leu Met				
245	250	255			
Asp Gly Ala Phe Trp Gly Leu Ser Asn	Met Glu Ile Leu Gln Leu				
260	265	270			
Asp His Asn Asn Leu Thr Glu Ile Thr	Lys Gly Trp Leu Tyr Gly				
275	280	285			
Leu Leu Met Leu Gln Glu Leu His Leu	Ser Gln Asn Ala Ile Asn				
290	295	300			
Arg Ile Ser Pro Asp Ala Trp Glu Phe	Cys Gln Lys Leu Ser Glu				
305	310	315			
Leu Asp Leu Thr Phe Asn His Leu Ser	Arg Leu Asp Asp Ser Ser				
320	325	330			
Phe Leu Gly Leu Ser Leu Leu Asn Thr	Leu His Ile Gly Asn Asn				
335	340	345			
Arg Val Ser Tyr Ile Ala Asp Cys Ala	Phe Arg Gly Leu Ser Ser				
350	355	360			
Leu Lys Thr Leu Asp Leu Lys Asn Asn	Glu Ile Ser Trp Thr Ile				
365	370	375			
Glu Asp Met Asn Gly Ala Phe Ser Gly	Leu Asp Lys Leu Arg Arg				
380	385	390			
Leu Ile Leu Gln Gly Asn Arg Ile Arg	Ser Ile Thr Lys Lys Ala				
395	400	405			
Phe Thr Gly Leu Asp Ala Leu Glu His	Leu Asp Leu Ser Asp Asn				
410	415	420			
Ala Ile Met Ser Leu Gln Gly Asn Ala	Phe Ser Gln Met Lys Lys				
425	430	435			
Leu Gln Gln Leu His Leu Asn Thr Ser	Ser Leu Leu Cys Asp Cys				
440	445	450			
Gln Leu Lys Trp Leu Pro Gln Trp Val	Ala Glu Asn Asn Phe Gln				
455	460	465			
Ser Phe Val Asn Ala Ser Cys Ala His	Pro Gln Leu Leu Lys Gly				
470	475	480			

Arg Ser Ile Phe	Ala Val Ser Pro Asp	Gly Phe Val Cys Asp Asp	485	490	495
Phe Pro Lys Pro	Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser Ala	500	505	510
Ile Lys Gly Ser	Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser Ser	515	520	525
Ser Asp Ser Pro	Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu Leu	530	535	540
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala Gln	545	550	555
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg Glu	560	565	570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser Asn	575	580	585
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val Asn	590	595	600
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile Arg	605	610	615
Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His Pro	620	625	630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe Pro	635	640	645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp Val	650	655	660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr Ser	665	670	675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala Thr	680	685	690
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu Asp	695	700	705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile Ala	710	715	720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp Ser	725	730	735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn Gln	740	745	750

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Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
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1115		

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&lt;211&gt; 18

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&lt;213&gt; Artificial Sequence

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&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

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&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

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&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe





<220>  
<223> Synthetic Oligonucleotide Probe

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gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

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<212> PRT

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Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg
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<210> 318

<211> 50

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<213> Homo Sapien

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His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
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Glu Asp Ala Leu	Asp Asp Phe Gly Ile	Tyr Glu Phe Val Ala	Phe		
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&lt;211&gt; 23

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&lt;213&gt; Artificial Sequence

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<213> Homo Sapien

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Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys	35	40	45	
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser	50	55	60	
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp	65	70	75	
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val	80	85	90	
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu	95	100	105	
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Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser	155	160	165	
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly	170	175	180	
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln	185	190	195	
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu	200	205	210	



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Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
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<213> Artificial Sequence

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<400> 333

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<210> 334

<211> 19

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 334

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<210> 335

<211> 19

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 335

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<210> 336

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<212> DNA

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<400> 336  
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His Gly Asp Glu	Arg Pro Ala Trp Leu	Met Ser Glu Thr Leu Arg			
	155	160			165
His Leu His Thr	His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile			
	170	175			180
Met Gln Asp Asp	Thr Tyr Val Gln Ala	Pro Arg Leu Ala Ala Leu			
	185	190			195
Ala Gly His Leu	Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala			
	200	205			210
Glu Glu Phe Ile	Gly Ala Gly Glu Gln	Ala Arg Tyr Cys His Gly			
	215	220			225
Gly Phe Gly Tyr	Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg			
	230	235			240
Pro His Leu Asp	Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro			
	245	250			255
Asp Glu Trp Leu	Gly Arg Cys Leu Ile	Asp Ser Leu Gly Val Gly			
	260	265			270
Cys Val Ser Gln	His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu			
	275	280			285
Ala Lys Asn Arg	Asp Pro Glu Lys Glu	Gly Ser Ser Ala Phe Leu			
	290	295			300
Ser Ala Phe Ala	Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr			
	305	310			315
Arg Leu His Lys	Arg Phe Ser Ala Leu	Glu Leu Glu Arg Ala Tyr			
	320	325			330
Ser Glu Ile Glu	Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val			
	335	340			345
Leu Thr Pro Glu	Gly Glu Ala Gly Leu	Ser Trp Pro Val Gly Leu			
	350	355			360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	620	625	630

Ser	Pro	Gln	Arg	Ser 635	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Gly	Pro	Asp 645
Pro	Pro	Ser	Pro	Pro 650	Gly	Ala	Asp	Pro	Ser	Arg	Gly	Ala	Pro	Ile 660
Gly	Gly	Arg	Phe	Asp 665	Arg	Gln	Ala	Ser	Ala	Glu	Gly	Cys	Phe	Tyr 675
Asn	Ala	Asp	Tyr	Leu 680	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu 690
Ala	Gly	Gln	Glu	Glu 695	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met 705
Asp	Val	Phe	Leu	Arg 710	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val 720
Glu	Pro	Gly	Leu	Val 725	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro 735
Arg	Leu	Ser	Glu	Glu 740	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu 750
Glu	Gly	Leu	Gly	Gly 755	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu 765
Gln	Glu	Gln	Ala	Asn 770	Ser	Thr								

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

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tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100

ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150

tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200

catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250

ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300

ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350

accaaact gtagaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450  
 aagcttaciaa atacgccttt gataagtata gagaccaata caactgggtc 500  
 ttccttgcaac gcccactac gtttgctatc attgaaaacc taaagtattt 550  
 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagtttgctt gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
 gatggaaaag atgtatttaa taccaaactc gttgggcttt ctattaaaga 850  
 ggcaatgact tatcacccca accaggtagt agaaggctgt tggtcagata 900  
 tggctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
 tatggggtat accgccttag ggcatttggg catattttca atgatgcatt 1000  
 ggttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
 agcgtgaata tgatctttgt ataggacgtg tggtgtcatt atttgtagta 1100  
 gtaactacat atccaatata gctgtatgtt tctttttctt ttctaatttg 1150  
 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaata 1200  
 ggggtggtttt tttctttaaa acacatgaac attgtaaatg tggtggaaag 1250  
 aagtgtttta agaataataa ttttgcaaact aaactattaa taaatattat 1300  
 atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350  
 tttgctgatt ggttaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400  
 gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450  
 tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctcccaa 1500  
 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550  
 attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien





	260		265		270
Cys Ser Asp Met	Ala Val Thr Phe Asn	Gly Leu Thr Pro Asn	Gln		
	275		280		285
Met His Val Met	Met Tyr Gly Val Tyr	Arg Leu Arg Ala Phe	Gly		
	290		295		300
His Ile Phe Asn Asp	Ala Leu Val Phe	Leu Pro Pro Asn	Gly Ser		
	305		310		315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

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<210> 343

<211> 18

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<223> Synthetic Oligonucleotide Probe

<400> 343

ctgggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaagtc cctaaggcgg tataacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

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TPP 20" 23440660

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<211> 25

<212> DNA

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<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatacgcactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

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<220>  
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<400> 350  
ggattctaatacgcactcactatagggcgccgatgtccactggggctac48

<210> 351  
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<400> 351  
ctatgaaattaacccctcactaaagggacgagggaagatgggcggatgggt48

<210> 352  
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<400> 352  
ggattctaatacgcactcactatagggcaccacgcgcgtccggctgctt47

<210> 353  
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<400> 353  
ctatgaaattaacccctcactaaagggacgggggacaccacggaccaga48

<210> 354  
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<400> 354  
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<210> 355  
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<400> 355  
ctatgaaatt aaccctcact aaaggagct gccgatccca ctggtatt 48

<210> 356  
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<400> 356  
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<210> 357  
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<400> 357  
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<210> 358  
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<400> 358  
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<210> 359  
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<400> 359  
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ggattctaatac gactcact atagggcccc tctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 365

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<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

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<210> 367

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<212> DNA

<213> Artificial Sequence

<220>

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<400> 367

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<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 368

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<210> 369

<211> 48

<212> DNA

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<223> Synthetic Oligonucleotide Probe

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<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

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<400> 370

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<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

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<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatt acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 373

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<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

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<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc caggatgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

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agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100

aaaaaatgaa ttcattctaaa tcattctgaaa cacaatgcac agagagagga 150

tgtttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200

attttctcagt gcctgtttca tcaccagatg tgttgatgaca tttcgcatct 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

ctctctctgct acaattatgg atcagggttca gtcaagaatt gttgtccatt 350

gaactgggaa tatttttcaat ccagctgcta cttcttttct actgacacca 400

tttctctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450

gtgggttatca actcacagga ggagcaggaa ttccttttct acaagaaacc 500

taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggtc 550

agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600

gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650

gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700

tcaattattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750



ggaaaatctc tttaagaaca gaaggcacia ctcaaattgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	20	25	30	
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	35	40	45	
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	50	55	60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	65	70	75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	80	85	90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	95	100	105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	110	115	120	
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	125	130	135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	140	145	150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	155	160	165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	170	175	180	

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
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<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

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<210> 379

<211> 24

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

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<211> 26

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

<210> 382  
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<400> 382  
ggccttgacg acaaccgt 18

<210> 383  
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<400> 383  
cagactgagg gagatccgag a 21

<210> 384  
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<220>  
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<400> 384  
cagctgccct tccccaacca 20

<210> 385  
<211> 18  
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<220>  
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<400> 385  
catcaagcgc ctctacca 18

<210> 386  
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<400> 386

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cacaaactcg aactgcttct g 21

<210> 387

<211> 18

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 387

gggccatcac agctccct 18

<210> 388

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gggatgtggt gaacacagaa ca 22

<210> 389

<211> 22

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 389

tgccagctgc atgctgccag tt 22

<210> 390

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence



<212> DNA  
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<220>  
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<210> 402  
<211> 22  
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<220>  
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<400> 402  
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<210> 403  
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<400> 403  
gccaaaggggtg gtgtagata gg 22

<210> 404  
<211> 24  
<212> DNA  
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<220>  
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<400> 404  
caggccccct tgatctgtac ccca 24

<210> 405  
<211> 23  
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<220>  
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<400> 405  
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gccaggcctc acattcgt 18

<210> 411

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 412

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

aggtgtttat taagggccta cgct 24

<210> 413

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 413

cagagcagag ggtgccttg 19

<210> 414

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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tggcggagtc ccctcttggc t 21

<210> 415

<211> 22

<212> DNA

<213> Artificial Sequence

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<220>  
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<210> 421  
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Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
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Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
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Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
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Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly
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Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					

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